

RAW SEQUENCE LISTING

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Application Serial Number: 10/735,991A
Source: IFW/6
Date Processed by STIC: 12/28/2005

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IFW16

RAW SEQUENCE LISTING

DATE: 12/28/2005

PATENT APPLICATION: US/10/735,991A

TIME: 12:17:45

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Output Set: N:\CRF4\12282005\J735991A.raw

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3 <110> APPLICANT: GOODNOW JR., ROBERT A.
4     MARK, DAVID F.
5     MARTIN, MITCHELL L.
6     ROSINSKI, JAMES A.
8 <120> TITLE OF INVENTION: SEQUENCE #115 AS A TARGET FOR IDENTIFYING WEIGHT
9     MODULATING COMPOUNDS
11 <130> FILE REFERENCE: 21366 US1
13 <140> CURRENT APPLICATION NUMBER: 10/735,991A
14 <141> CURRENT FILING DATE: 2003-12-15
16 <150> PRIOR APPLICATION NUMBER: 60/436,375
17 <151> PRIOR FILING DATE: 2002-12-23
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: PatentIn Ver. 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1014
25 <212> TYPE: DNA
26 <213> ORGANISM: Mus musculus
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31 ccggcgctct tcaactctcaa cctcacgtgt ggcaacctgc tgtgtaccgt ggtcaacatg 180
32 ccaactaacac tggccggcgt cgtggcacaa cggcagccgg ccggggaccg cctgtgccgc 240
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40 caccacagtg tgagggaacg gtgtctggag gaacagaagc ggaggcgaca gcgtgccacc 720
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49 <211> LENGTH: 337
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60 Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
61          35          40          45
63 Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
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66 Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
67 65          70          75          80
69 Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser
70          85          90          95
72 Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu
73          100          105          110
75 Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Phe Met Val Ala
76          115          120          125
78 Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu
79          130          135          140
81 Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser
82 145          150          155          160
84 Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe
85          165          170          175
87 His Ala Leu Ser Phe Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr
88          180          185          190
90 Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val
91          195          200          205
93 Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Ile His Pro Ser Val
94          210          215          220
96 Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr
97 225          230          235          240
99 Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro
100          245          250          255
102 Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Gly
103          260          265          270
105 Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala
106          275          280          285
108 Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Arg Ser
109          290          295          300
111 Cys Lys Glu Leu Leu Asn Arg Ile Phe Asn Arg Arg Ser Leu His Ser
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129 acagcgctga catcgcgcg caggcgccgg cgctcttcac tctcaacctc acgtgtggca 180
130 acctgctgtg taccgtgggtc aacatgccac taacactggc cggcgctcgtg gcacaacggc 240

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132 actccatgct cagtatggcc gcgctcagca tcgaccgctg ggtggctgtg gtcttcccgc 360
133 tgagctaccg tgccaagatg cgctccgag atgcccctt catggtggcc tacacgtggc 420
134 tgcacgcgct caccttcccc gccaccgcgc tcgcctgtc ctggctcggc ttccaccagc 480
135 tgtatgcctc gtgcacgctg tgcagccggc ggcccagca gcgcctgcgc ttgctgtct 540
136 tcaccagcgc cttccatgcg cttagcttcc tgctctcctt catcgtgctc tgcttcacgt 600
137 acctcaaggt gctcaaggtg gcccgtttcc actgcaagcg catcgacgtg atcaccatgc 660
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142 tcgtgtactc cttgctgcga caccagtacc gcaggagctg caaggagctt ctgaacagga 960
143 tcttcaacag acgctccatt cactctgtgg gcctcacagg tgactctcac agccagaaca 1020
144 ttctgccagt gtcggaatga aggacagctc tctgttgagg gagttcagaa tgaggtggcc 1080
145 agagcagagg gaggtggtct gggactcctg ggtggacagg aactgccacc attgtctggc 1140
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149 <210> SEQ ID NO: 4

150 <211> LENGTH: 337

151 <212> TYPE: PRT

152 <213> ORGANISM: Rattus norvegicus

154 <400> SEQUENCE: 4

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158 Gly Val Ser Leu Leu Ser Asn Gly Leu Val Leu Leu Cys Leu Leu His
159           20           25           30
161 Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
162           35           40           45
164 Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
165           50           55           60
167 Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
168   65           70           75           80
170 Leu Ala Ala Phe Leu Asp Thr Phe Leu Ala Ala Asn Ser Met Leu Ser
171           85           90           95
173 Met Ala Ala Leu Ser Ile Asp Arg Trp Val Ala Val Val Phe Pro Leu
174           100          105          110
176 Ser Tyr Arg Ala Lys Met Arg Leu Arg Asp Ala Ala Phe Met Val Ala
177           115          120          125
179 Tyr Thr Trp Leu His Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu
180           130          135          140
182 Ser Trp Leu Gly Phe His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser
183 145           150          155          160
185 Arg Arg Pro Asp Glu Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe
186           165          170          175
188 His Ala Leu Ser Phe Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr
189           180          185          190
191 Leu Lys Val Leu Lys Val Ala Arg Phe His Cys Lys Arg Ile Asp Val
192           195          200          205
194 Ile Thr Met Gln Thr Leu Val Leu Leu Val Asp Ile His Pro Ser Val
195           210          215          220

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197 Arg Glu Arg Cys Leu Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr
198 225                230                235                240
200 Lys Lys Ile Ser Thr Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro
201                245                250                255
203 Tyr Val Ile Thr Arg Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Asp
204                260                265                270
206 Ser His Trp Gly Val Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala
207                275                280                285
209 Ser Asp Pro Phe Val Tyr Ser Leu Leu Arg His Gln Tyr Arg Arg Ser
210                290                295                300
212 Cys Lys Glu Leu Leu Asn Arg Ile Phe Asn Arg Arg Ser Ile His Ser
213 305                310                315                320
215 Val Gly Leu Thr Gly Asp Ser His Ser Gln Asn Ile Leu Pro Val Ser
216                325                330                335
218 Glu
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 1014
224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
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230 ccggcgctct tcacctgaa cctcacgtgc gggaacctgc tgtgcaccgt ggtcaacatg 180
231 ccgtcacgc tggccggcgt cgtggcgcgag cggcagccgg cgggcgaccg cctgtgccgc 240
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233 agcatcgacc gctgggtggc cgtggtcttc ccgctgagct accggggccaa gatgcgcctc 360
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239 caccacagtg tgcgggaacg ctgtctggag gagcagaagc ggaggcgaca gcgagccacc 720
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243 taccgcaaaa gctgcaagga gattctgaac aggctcctgc acagacgctc catccactcc 960
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248 <211> LENGTH: 337
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
252 <400> SEQUENCE: 6
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257 20 25 30
259 Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
260 35 40 45
262 Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu

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VERIFICATION SUMMARY

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